SEQUENCE LISTING

<110> Hisashi NARIMATSU

Akira TOGAYACHI

Niro INABA

Toru HIRUMA

Yasuko ISHIZUKA

NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY

<120> BETA1,3-N-ACETYL-D-GALACTOSAMINE TRANSFERASE PROTEIN, NUCLEIC ACID ENCODING THE SAME AND METHOD OF EXAMINING CANCERATION USING THE SAME

<130> 159-90 / PC/S-84-6

<140> US 10/539,450

<141> 2005-12-06

<150> PCT/JP2004/000608

<151> 2004-01-23

<150> JP 392555/2003

<151> 2003-11-21

<150> JP 285310/2003

<151> 2003-08-01

<150> JP 014792/2003

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<210> 2

<211> 500

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<213> Homo sapiens

<400> 2

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1 5 10 15

Leu His Leu Trp Leu Arg Leu Arg Ser Pro Pro Pro Ala Cys Ala Ser

20 25 30

Gly Ala Gly Pro Ala Asp Gln Leu Ala Leu Phe Pro Gln Trp Lys Ser

35 40 45

Thr His Tyr Asp Val Val Gly Val Leu Ser Ala Arg Asn Asn His
50 55 60

Glu Leu Arg Asn Val Ile Arg Ser Thr Trp Met Arg His Leu Leu Gln
65 70 75 80

His Pro Thr Leu Ser Gln Arg Val Leu Val Lys Phe Ile Ile Gly Ala 85 90 95

His Gly Cys Glu Val Pro Val Glu Asp Arg Glu Asp Pro Tyr Ser Cys

100 105 110

Lys Leu Leu Asn Ile Thr Asn Pro Val Leu Asn Gln Glu Ile Glu Ala
115 120 125

Phe Ser Leu Ser Glu Asp Thr Ser Ser Gly Leu Pro Glu Asp Arg Val

130 135 140

Val Ser Val Ser Phe Arg Val Leu Tyr Pro Ile Val Ile Thr Ser Leu

145 150 155 160

Gly Val Phe Tyr Asp Ala Asn Asp Val Gly Phe Gln Arg Asn Ile Thr

165 170 175

Val Lys Leu Tyr Gln Ala Glu Gln Glu Glu Ala Leu Phe Ile Ala Arg

180 185 190

Phe Ser Pro Pro Ser Cys Gly Val Gln Val Asn Lys Leu Trp Tyr Lys

195 200 205

Pro Val Glu Gln Phe Ile Leu Pro Glu Ser Phe Glu Gly Thr Ile Val
210 215 220

Trp Glu Ser Gln Asp Leu His Gly Leu Val Ser Arg Asn Leu His Lys
225 230 235 240

Val Thr Val Asn Asp Gly Gly Gly Val Leu Arg Val Ile Thr Ala Gly

245 250 255

Glu Gly Ala Leu Pro His Glu Phe Leu Glu Gly Val Glu Gly Val Ala
260 265 270

Gly Gly Phe Ile Tyl hr Ile Gln Glu Gly Asp Ala Leu Leu His Asn 275 280 285

•

Leu His Ser Arg Pro Gln Arg Leu Ile Asp His Ile Arg Asn Leu His
290 295 300

Glu Glu Asp Ala Leu Leu Lys Glu Glu Ser Ser Ile Tyr Asp Asp Ile 305 310 315 320

Val Phe Val Asp Val Val Asp Thr Tyr Arg Asn Val Pro Ala Lys Leu
325 330 335

Leu Asn Phe Tyr Arg Trp Thr Val Glu Thr Thr Ser Phe Asn Leu Leu 340 345 350

Leu Lys Thr Asp Asp Asp Cys Tyr Ile Asp Leu Glu Ala Val Phe Asn 355 360 365

Arg Ile Val Gln Lys Asn Leu Asp Gly Pro Asn Phe Trp Trp Gly Asn 370 375 380

Phe Arg Leu Asn Trp Ala Val Asp Arg Thr Gly Lys Trp Gln Glu Leu 385 390 395 400

Glu Tyr Pro Ser Pro Ala Tyr Pro Ala Phe Ala Cys Gly Ser Gly Tyr
405 410 415

Val Ile Ser Lys Asp Ile Val Lys Trp Leu Ala Ser Asn Ser Gly Arg
420 425 430

Leu Lys Thr Tyr Gla Asp Val Ser Met Gly Ile Trp Met Ala
435 440 445

Ala Ile Gly Pro Lys Arg Tyr Gln Asp Ser Leu Trp Leu Cys Glu Lys
450 455 460

Thr Cys Glu Thr Gly Met Leu Ser Ser Pro Gln Tyr Ser Pro Trp Glu
465 470 475 480

Leu Thr Glu Leu Trp Lys Leu Lys Glu Arg Cys Gly Asp Pro Cys Arg
485 490 495

Cys Gln Ala Arg

500

<210> 3

<211> 1515

<212> DNA

<213> Mouse

<400> 3

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ggaggccctt ttcatcgccc gattcagtcc tccaagttgt 600 ttgtatcaga cagagcag ggcgtacaag tgaacaagct ctggtataag cccgtggaac agttcatctt accagagagc 660 tttgaaggta caatcgtgtg ggaaagccaa gatctccatg gcctcgtgtc cagaaacctg 720 cacagagtga cagtgaatga tggaggggt gttctcagag tccttgcagc tggggaaggg 780 gcactgcctc atgaattcat ggaaggtgtg gagggagttg cgggtggctt tatctacact 840 gttcaggaag gtgatgcact attaagaagc ctttattctc ggccccagag acttgcagat 900 cacatacagg atctgcaggt ggaagatgcc ttactgcagg aggaaagcag tgtccatgac 960 gacattgtct tcgtggatgt tgtggatact taccggaatg ttcctgcaaa attactgaac 1020 ttctatagat ggactgtgga atccaccage ttcgatttgc tgctcaagac agatgacgac 1080 tgttatatag acttagaagc tgtgtttaat agaattgctc agaagaatct agatgggcct 1140 aatttttggt ggggaaattt caggttgaat tgggcagtgg acagaaccgg aaaatggcag 1200 gagctggaat acccgagccc ggcttaccct gcctttgcat gtgggtcagg gtatgtgatc 1260 tccaaggata tcgttgactg gctggcaggc aactccagaa ggttaaagac ctatcagggt 1320 gaagatgtca gcatgggcat ttggatggca gccataggac ctaaaagaca ccaggacagc 1380 ctgtggctgt gtgagaaaac ctgtgagaca ggaatgctgt cttctcctca gtactcacca 1440 gaagagctga gcaaactctg ggaactgaag gagctgtgtg gggatccttg tcagtgtgaa 1500 1515 gcaaaagtac gatga

<210> 4

<211> 504

<212> PRT

<213> Mouse

<400> 4

Met Arg Asn Trp Leu Val Leu Cys Pro Cys Val Leu Gly Ala Ala

1 5 10 15

Leu His Leu Trp His Leu Trp Leu Arg Ser Pro Pro Asp Pro His Asn
20 25 30

Thr Gly Pro Ser Ala Ma Asp Gln Ser Ala Leu Phe Pro His Trp Lys Phe Ser His Tyr Asp Val Val Val Gly Val Leu Ser Ala Arg Asn Asn His Glu Leu Arg Asn Val Ile Arg Asn Thr Trp Leu Lys Asn Leu Leu His His Pro Thr Leu Ser Gln Arg Val Leu Val Lys Phe Ile Ile Gly Ala Arg Gly Cys Glu Val Pro Val Glu Asp Arg Glu Asp Pro Tyr Ser Cys Arg Leu Leu Asn Ile Thr Asn Pro Val Leu Asn Gln Glu Ile Glu Ala Phe Ser Phe Pro Glu Asp Ala Ser Ser Ser Arg Leu Ser Glu Asp Arg Val Val Ser Val Ser Phe Arg Val Leu Tyr Pro Ile Val Ile Thr

•

Ser Leu Gly Val Phe Tyr Asp Ala Ser Asp Val Gly Phe Gln Arg Asn
. 165 170 175

Ile Thr Val Lys Leu Tyr Gln Thr Glu Glu Glu Ala Leu Phe Ile

180 185 190

Ala Arg Phe Ser Pro ro Ser Cys Gly Val Gln Val Asn Lys Leu Trp

195 200 205

• .

Tyr Lys Pro Val Glu Gln Phe Ile Leu Pro Glu Ser Phe Glu Gly Thr
210 215 220

Ile Val Trp Glu Ser Gln Asp Leu His Gly Leu Val Ser Arg Asn Leu
225 230 235 240

His Arg Val Thr Val Asn Asp Gly Gly Val Leu Arg Val Leu Ala
245 250 255

Ala Gly Glu Gly Ala Leu Pro His Glu Phe Met Glu Gly Val Glu Gly
260 265 270

Val Ala Gly Gly Phe Ile Tyr Thr Val Gln Glu Gly Asp Ala Leu Leu
275 280 285

Arg Ser Leu Tyr Ser Arg Pro Gln Arg Leu Ala Asp His Ile Gln Asp
290 295 300

Leu Gln Val Glu Asp Ala Leu Leu Gln Glu Glu Ser Ser Val His Asp
305 310 315 320

Asp Ile Val Phe Val Asp Val Val Asp Thr Tyr Arg Asn Val Pro Ala
325 330 335

Lys Leu Leu Asn Phe Tyr Arg Trp Thr Val Glu Ser Thr Ser Phe Asp 340 345 350

Leu Leu Leu Lys Thi sp Asp Cys Tyr Ile Asp Leu Glu Ala Val

• •

Phe Asn Arg Ile Ala Gln Lys Asn Leu Asp Gly Pro Asn Phe Trp Trp 370 375 380

Gly Asn Phe Arg Leu Asn Trp Ala Val Asp Arg Thr Gly Lys Trp Gln
385 390 395 400

Glu Leu Glu Tyr Pro Ser Pro Ala Tyr Pro Ala Phe Ala Cys Gly Ser
405 410 415

Gly Tyr Val Ile Ser Lys Asp Ile Val Asp Trp Leu Ala Gly Asn Ser
420 425 430

Arg Arg Leu Lys Thr Tyr Gln Gly Glu Asp Val Ser Met Gly Ile Trp
435 440 445

Met Ala Ala Ile Gly Pro Lys Arg His Gln Asp Ser Leu Trp Leu Cys
450 455 460

Glu Lys Thr Cys Glu Thr Gly Met Leu Ser Ser Pro Gln Tyr Ser Pro 465 470 475 480

Glu Glu Leu Ser Lys Leu Trp Glu Leu Lys Glu Leu Cys Gly Asp Pro
485 490 495

Cys Gln Cys Glu Ala Lys Val Arg

<210> 5 <211> 37 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: 5' primer for PCR <400> 5 37 cccaagcttg ggcctgcaga tcagttggcc ttatttc <210> 6 <211> 42 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: 3' primer for PCR <400> 6 42 aacgcggatc cgcgctgtta tcttgcttga catcgacaag ga <210> 7

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5' primer for PCR

<400> 7 ggggacaagt ttgtacaaaa aagcaggctt ccctgcagat cagttggcct tatttc 56 <210> 8 <211> 58 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: 3' primer for PCR <400> 8 ggggaccact ttgtacaaga aagctgggtc ctgttatctt gcttgacatc gacaagga 58 <210> 9 <211> 22 <212> PRT <213> Artificial Sequence <220>

<400> 9
Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

<223> Description of Artificial Sequence: Igkappa signal sequence

Val Ile Met Ser Arg Gly

20

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<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: FLAG peptide
<400> 10
Asp Tyr Lys Asp Asp Asp Lys
<210> 11
<211> 94
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer OT3
<400> 11
gatcatgcat tttcaagtgc agattttcag cttcctgcta atcagtgcct cagtcataat 60
gtcacgtgga gattacaagg acgacgatga caag
                                                                   94
<210> 12
<211> 26
<212> DNA
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- 13 -

<213> Artificial Sequence

| <220> | | |
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| <223> | Description of Artificial Sequence: primer OT20 | |
| | | |
| <400> | 12 | |
| cgggat | tccat gcattttcaa gtgcag | 26 |
| | | |
| | | |
| <210> | 13 | |
| <211> | 25 | |
| <212> | DNA | |
| <213> | Artificial Sequence | |
| | | |
| <220> | | |
| <223> | Description of Artificial Sequence: primer OT21 | |
| | | |
| <400> | 13 | |
| ggaatt | ccttg tcatcgtcgt ccttg | 25 |
| | | |
| | | |
| <210> | 14 | |
| <211> | 21 | |
| <212> | DNA | |
| <213> | Artificial Sequence | |
| | | |
| <220> | | |
| <223> | Description of Artificial Sequence: 5' primer for PCR | |
| | | |
| <400> | 14 | |

ggagtgttct acgatgccaa t

21

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: 3' primer for PCR
<400> 15
ctgaagcgag caatgaagag 20

<210> 16 <211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TaqMan Probe

<400> 16

cactgtcaaa ctttatcagg cagaacaaga gg 32

<210> 17

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

223> Description Artificial Sequence: 5' primer for PCR

<400> 17

cccaagcttg ggagcgcggc agatcaatca gccttat 37

<210> 18

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 3' primer for PCR

<400> 18

ttttcctttt gcggccgctt ttttcctttc atcgtacttt tgcttcacac tga 53

<210> 19

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<223> b3Gal-T1

<400> 19

Phe Leu Val Ile Leu Ile Ser Thr Thr His Lys Glu Phe Asp Ala Arg

1 5 10 15

Gln Ala Ile Arg Gla rhr Trp Gly Asp Glu Asn Asn Phe Lys Gly Ile
20 25 30

.*.

Lys Ile Ala Thr Leu Phe Leu Leu Gly Lys Asn Ala Asp Pro Val Leu

35 40 45

Asn Gln Met Val Glu Gln Glu Ser Gln Ile Phe His Asp Ile Ile Val
50 55 60

Glu Asp Phe Ile Asp Ser Tyr His Asn Leu Thr Leu Lys Thr Leu Met

70, 75 80

Gly Met Arg Trp Val Ala Thr Phe Cys Ser Lys Ala Lys Tyr Val Met

85 90 95

Lys Thr Asp Ser Asp Ile Phe Val Asn Met Asp Asn Leu Ile Tyr Lys

100 105 110

Leu Leu Lys Pro Ser Thr Lys Pro Arg Arg Tyr Phe Thr Gly Tyr

115 120 125

Val Ile Asn Gly Gly Pro Ile Arg Asp Val Arg Ser Lys Trp Tyr Met

130 135 140

Pro Arg Asp Leu Tyr Pro Asp Ser Asn Tyr Pro Pro Phe Cys Ser Gly
145 150 155 160

Thr Gly Tyr Ile Phe Ser Ala Asp Val Ala Glu Leu Ile Tyr Lys Thr

165 170 175

Ser Leu His Thr Arg Leu Leu His Leu Glu Asp Val Tyr Val Gly Leu
180 185 190

Ser Leu His Thr Arg Leu Leu His Leu Glu Asp Val Tyr Val Gly Leu
195 200 205

His Trp Lys Met Ala Tyr Ser Leu Cys Arg Tyr Arg Arg Val Ile Thr
210 215 220

Val His Gln Ile Ser Pro Glu Glu Met His Arg Ile Trp Asn Asp Met
225 230 235 240

Ser Ser Lys Lys His Leu Arg Cys

245

<210> 20

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<211> 271

<212> PRT

<213> Homo sapiens

<220>

<223> b3Gal-T2

<400> 20

Phe Leu Ile Leu Leu Ile Ala Ala Glu Pro Gly Gln Ile Glu Ala Arg

1 5 10 15

Arg Ala Ile Arg Gln Thr Trp Gly Asn Glu Ser Leu Ala Pro Gly Ile
20 25 30

Gln Ile Thr Arg Ile Phe Leu Leu Gly Leu Ser Ile Lys Leu Asn Gly
35 40 45

.* 4

Tyr Leu Gln Arg Ala Ile Leu Glu Glu Ser Arg Gln Tyr His Asp Ile
50 55 60

Ile Gln Gln Glu Tyr Leu Asp Thr Tyr Tyr Asn Leu Thr Ile Lys Thr

70 75 80

Leu Met Gly Met Asn Trp Val Ala Thr Tyr Cys Pro His Ile Pro Tyr

85
90
95

Val Met Lys Thr Asp Ser Asp Met Phe Val Asn Thr Glu Tyr Leu Ile

100 105 110

Asn Lys Leu Leu Lys Pro Asp Leu Pro Pro Arg His Asn Tyr Phe Thr
115 120 125

Gly Tyr Leu Met Arg Gly Tyr Ala Pro Asn Arg Asn Lys Asp Ser Lys

130 135 140

Trp Tyr Met Pro Pro Asp Leu Tyr Pro Ser Glu Arg Tyr Pro Val Phe
145 150 155 160

Cys Ser Gly Thr Gly Tyr Val Phe Ser Gly Asp Leu Ala Glu Lys Ile

165 170 175

Phe Lys Val Ser Leu Gly Ile Arg Arg Leu His Leu Glu Asp Val Tyr

180 185 190

Val Gly Ile Cys Let Ala Lys Leu Arg Ile Asp Pro Val Pro Pro Pro 195 200 205

Asn Glu Phe Val Phe Asn His Trp Arg Val Ser Tyr Ser Ser Cys Lys
210 215 220

Tyr Ser His Leu Ile Thr Ser His Gln Phe Gln Pro Ser Glu Leu Ile
225 230 235 240

Lys Tyr Trp Asn His Leu Gln Gln Asn Lys His Asn Ala Cys Ala Asn
245
250
255

Ala Ala Lys Glu Lys Ala Gly Arg Tyr Arg His Arg Lys Leu His
260 265 270

<210> 21

•..

<211> 253

<212> PRT

<213> Homo sapiens

<220>

<223> b3Gal-T3

<400> 21

Phe Leu Val Ile Leu Val Thr Ser His Pro Ser Asp Val Lys Ala Arg

1 5 10 15

Gln Ala Ile Arg Val Thr Trp Gly Glu Lys Lys Ser Trp Trp Gly Tyr

20 25 30

Glu Val Leu Thr Phe Phe Leu Leu Gly Gln Glu Ala Glu Lys Glu Asp
35 40 45

(M)

Lys Met Leu Ala Leu Ser Leu Glu Asp Glu His Leu Leu Tyr Gly Asp
50 55 60

Ile Ile Arg Gln Asp Phe Leu Asp Thr Tyr Asn Asn Leu Thr Leu Lys

70

75

80

Thr Ile Met Ala Phe Arg Trp Val Thr Glu Phe Cys Pro Asn Ala Lys

85 90 95

Tyr Val Met Lys Thr Asp Thr Asp Val Phe Ile Asn Thr Gly Asn Leu
100 105 110

Val Lys Tyr Leu Leu Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly
115 120 125

Tyr Pro Leu Ile Asp Asn Tyr Ser Tyr Arg Gly Phe Tyr Gln Lys Thr

130 135 140

Ser Gly Leu Gly Tyr Ile Met Ser Arg Asp Leu Val Pro Arg Ile Tyr

165 170 175

Glu Met Met Gly His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val
180 185 190

Gly Ile Cys Leu Ash Leu Leu Lys Val Asn Ile His Ile Pro Glu Asp

Thr Asn Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys Gln Leu 210 215 220

Arg Arg Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu Ile Ile Thr
225 230 235 240

Phe Trp Gln Val Met Leu Arg Asn Thr Thr Cys His Tyr
245 250

<210> 22

<211> 253

<212> PRT

<213> Homo sapiens

<220>

<223> b3Gal-T5

<400> 22

Phe Leu Val Leu Leu Val Thr Ser Ser His Lys Gln Leu Ala Glu Arg

1 5 10 15

Met Ala Ile Arg Gln Thr Trp Gly Lys Glu Arg Met Val Lys Gly Lys
20 25 30

Gln Leu Lys Thr Phe Phe Leu Leu Gly Thr Thr Ser Ser Ala Ala Glu 35 40 45

Thr Lys Glu Val Asp Gln Glu Ser Gln Arg His Gly Asp Ile Ile Gln Lys Asp Phe Leu Asp Val Tyr Tyr Asn Leu Thr Leu Lys Thr Met Met Gly Ile Glu Trp Val His Arg Phe Cys Pro Gln Ala Ala Phe Val Met Lys Thr Asp Ser Asp Met Phe Ile Asn Val Asp Tyr Leu Thr Glu Leu Leu Leu Lys Lys Asn Arg Thr Thr Arg Phe Phe Thr Gly Phe Leu Lys Leu Asn Glu Phe Pro Ile Arg Gln Pro Phe Ser Lys Trp Phe Val Ser Lys Ser Glu Tyr Pro Trp Asp Arg Tyr Pro Pro Phe Cys Ser Gly Thr Gly Tyr Val Phe Ser Gly Asp Val Ala Ser Gln Val Tyr Asn Val Ser

Gly Tyr Val Phe Ser Gly Asp Val Ala Ser Gln Val Tyr Asn Val Ser 165 170 175

Lys Ser Val Pro Tyr Ile Lys Leu Glu Asp Val Phe Val Gly Leu Cys

180 185 190

Leu Glu Arg Leu Asn Ile Arg Leu Glu Glu Leu His Ser Gln Pro Thr
195 200 205

Phe Phe Pro Gly Gly

eu Arg Phe Ser Val Cys Leu Phe Arg Arg Ile 220 210 215

Val Ala Cys His Phe Ile Lys Pro Arg Thr Leu Leu Asp Tyr Trp Gln 225 230 235 240

Ala Leu Glu Asn Ser Arg Gly Glu Asp Cys Pro Pro Val 245 250

<210> 23

<211> 272

<212> PRT

<213> Homo sapiens

<220>

<223> b3Gal-T6

<400> 23

Phe Leu Ala Val Leu Val Ala Ser Ala Pro Arg Ala Ala Glu Arg Arg 15 5 10

Ser Val Ile Arg Ser Thr Trp Leu Ala Arg Arg Gly Ala Pro Gly Asp 30 20 25

Val Trp Ala Arg Phe Ala Val Gly Thr Ala Gly Leu Gly Ala Glu Glu 45 40 35

Arg Arg Ala Leu Glu Arg Glu Gln Ala Arg His Gly Asp Leu Leu 55 60 50

Leu Pro Ala Leu Arg Asp Ala Tyr Glu Asn Leu Thr Ala Lys Val Leu 65 70 75 80

Ala Met Leu Ala Trp Leu Asp Glu His Val Ala Phe Glu Phe Val Leu 85 90 95

Lys Ala Asp Asp Asp Ser Phe Ala Arg Leu Asp Ala Leu Leu Ala Glu

100 105 110

Leu Arg Ala Arg Glu Pro Ala Arg Arg Arg Leu Tyr Trp Gly Phe
115 120 125

Phe Ser Gly Arg Gly Arg Val Lys Pro Gly Gly Arg Trp Arg Glu Ala
130 135 140

Ala Trp Gln Leu Cys Asp Tyr Tyr Leu Pro Tyr Ala Leu Gly Gly
145 150 155 160

Tyr Val Leu Ser Ala Asp Leu Val His Tyr Leu Arg Leu Ser Arg Asp

165 170 175

Tyr Leu Arg Ala Trp His Ser Glu Asp Val Ser Leu Gly Ala Trp Leu
180 185 190

Ala Pro Val Asp Val Gln Arg Glu His Asp Pro Arg Phe Asp Thr Glu
195 200 205

Tyr Arg Ser Arg Gly Cys Ser Asn Gln Tyr Leu Val Thr His Lys Gln
210 215 220

Ser Leu Glu Asp Met eu Glu Lys His Ala Thr Leu Ala Arg Glu Gly
225 230 235 240

Arg Leu Cys Lys Arg Glu Val Gln Leu Arg Leu Ser Tyr Val Tyr Asp
245 250 255

Trp Ser Ala Pro Pro Ser Gln Cys Cys Gln Arg Arg Glu Gly Ile Pro
260 265 270

<210> 24

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<223> b3GnT2

<400> 24

Phe Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg

1 5 10 15

Gln Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln
20 25 30

Thr Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn 35 40 45

His Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln 50 55 60

Asp Ile Leu Met Trousn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu 65 70 75 80

Lys Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr

85 90 95

Glu Phe Val Phe Lys Gly Asp Asp Val Phe Val Asn Thr His His

100 105 110

Ile Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu
115 120 125

Phe Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys
130 135 140

Leu Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro 145 150 155 160

Tyr Ala Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg

165 170 175

Leu Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val
180 185 190

Tyr Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His

195 200 205

Lys Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile
210 215 220

Cys Ser Tyr Val Asp. Leu Met Leu Val His Ser Arg Lys Pro Gln Glu

225 230 235 240

Met Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
245 250 255

<210> 25

<211> 265

<212> PRT

<213> Homo sapiens

<220>

<223> b3GnT3

<400> 25

Phe Leu Leu Val Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg

1 5 10 15

Glu Leu Leu Arg Arg Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu
20 25 30

Gln Leu Arg Leu Leu Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu
35 40 45

Ala Arg Lys Val Asn Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly
50 55 60

Asp Ile Leu Gln Trp Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu 65 70 75 80

Lys Gln Val Leu Phe Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala 85 90 95

Ser Phe Val Leu Asn Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn

100 105 110

Met Val Phe Tyr Leu Gln Asp His Asp Pro Gly Arg His Leu Phe Val

115 120 125

Gly Gln Leu Ile Gln Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys

130 135 140

Cys Gly Gly Gly Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu
165 170 175

Arg Arg Ala Ala His Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe
180 185 190

Leu Gly Met Cys Leu Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser

195 200 205

Gly Ile Arg Thr Ser Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser
210 215 220

Phe Asp Pro Cys Phe Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu 225 230 235 240

Pro Tyr Glu Met Leu Zeu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu
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Thr Cys Gly Asn Gln Thr Gln Ile Tyr
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20 25 30

Arg Gln Leu Lys Leu Val Phe Leu Leu Gly Val Ala Gly Ser Ala Pro
35 40 45

Pro Ala Gln Leu Leu Ala Tyr Glu Ser Arg Glu Phe Asp Asp Ile Leu
50 55 60

Gln Trp Asp Phe Thr Glu Asp Phe Phe Asn Leu Thr Leu Lys Glu Leu 65 70 75 80

Leu Lys Gly Asp Asp Val Phe Val His Val Pro Asn Val Leu Glu
100 105 110

Phe Leu Asp Gly Trp Asp Pro Ala Gln Asp Leu Leu Val Gly Asp Val
115 120 125

Ile Arg Gln Ala Leu Pro Asn Arg Asn Thr Lys Val Lys Tyr Phe Ile
130 135 140

Pro Pro Ser Met Tyr Arg Ala Thr His Tyr Pro Pro Tyr Ala Gly Gly

145 150 155 160

Gly Gly Tyr Val Met Ser Arg Ala Thr Val Arg Arg Leu Gln Ala Ile

165 170 175

Met Glu Asp Ala Glu Leu Phe Pro Ile Asp Asp Val Phe Val Gly Met
180 185 190

Cys Leu Arg Arg Leu Gly Leu Ser Pro Met His His Ala Gly Phe Lys

195 200 205

Thr Phe Gly Ile Arg Arg Pro Leu Asp Pro Leu Asp Pro Cys Leu Tyr
210 215 220

Arg Gly Leu Leu Leu Val His Arg Leu Ser Pro Leu Glu Met Trp Thr
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Met Trp Ala Leu Val

Thr Asp Glu Gly Leu Lys Cys Ala Ala Gly Pro 245 250 255

Ile Pro Gln Arg

260

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Ser Gly Ile Arg Arg Thr Trp Gly Asn Glu Asn Tyr Val Arg Ser Gln 20 25 30

Leu Asn Ala Asn Ile Lys Thr Leu Phe Ala Leu Gly Thr Pro Asn Pro 35 40 45

Leu Glu Gly Glu Glu Leu Gln Arg Lys Leu Ala Trp Glu Asp Gln Arg 60 50 55

Tyr Asn Asp Ile Ile Gln Gln Asp Phe Val Asp Ser Phe Tyr Asn Leu 80 65 70 75

His Ala Lys Phe Leu Met Thr Ala Asp Asp Ile Phe Ile His Met
100 105 110

Pro Asn Leu Ile Glu Tyr Leu Gln Ser Leu Glu Gln Ile Gly Val Gln
115 120 125

Asp Phe Trp Ile Gly Arg Val His Arg Gly Ala Pro Pro Ile Arg Asp
130 135 140

Tyr Pro Asp Tyr Thr Ala Gly Ala Ala Tyr Val Ile Ser Gly Asp Val

165 170 175

Ala Ala Lys Val Tyr Glu Ala Ser Gln Thr Leu Asn Ser Ser Leu Tyr

180 185 190

Ile Asp Asp Val Phe Met Gly Leu Cys Ala Asn Lys Ile Gly Ile Val
195 200 205

Pro Gln Asp His Val Phe Phe Ser Gly Glu Gly Lys Thr Pro Tyr His
210 215 220

Pro Cys Ile Tyr Glu Lys Met Met Thr Ser His Gly His Leu Glu Asp
225 230 235 240

Leu Gln Asp Leu Trp Lys Asn Ala Thr Asp Pro Lys Val Lys Thr Ile

245 250 255

Ser Lys Gly Phe Phe Gly Gln Ile Tyr Cys Arg Leu Met Lys Ile Ile
260 265 270

Leu Leu Cys Lys Ile Ser Tyr Val Asp Thr Tyr Pro Cys Arg Ala Ala 275 280 285

Phe Ile

290